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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/090,672ADATE: 01/05/2000
TIME: 04:16:25

INPUT SET: S34368.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: Ishiwata, Tetsuyoshi; Sakurada, Mikiko; Nishimura,
5 Ayako; Nakagawa, Satoshi; Nishi, Tatsunari; Kuga, Tetsuro; Sawada,
6 Shigemasa; Takei, Masami
7 (ii) TITLE OF INVENTION: IgA Nephropathy-Related Genes
8 (iii) NUMBER OF SEQUENCES: 111
9 (iv) CORRESPONDENCE ADDRESS:
10 (A) ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
11 (B) STREET: 30 Rockefeller Plaza
12 (C) CITY: New York
13 (D) STATE: New York
14 (E) ZIP: 10112-3801
15 (v) COMPUTER READABLE FORM:
16 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
17 (B) COMPUTER: Compac PC
18 (C) OPERATING SYSTEM: Windows 95
19 (D) SOFTWARE: WordPerfect 8.0
20 (vi) CURRENT APPLICATION DATA:
21 (A) APPLICATION NUMBER: 09/090,672
22 (B) FILING DATE: 04-JUNE-1998
23 (C) CLASSIFICATION: 435
24 (vii) PRIOR APPLICATION DATA:
25 (A) APPLICATION NUMBER: PCT/JP97/04468
26 (B) FILING DATE: 05-DEC-1997
27 (A) APPLICATION NUMBER: JP-8-325763
28 (B) FILING DATE: 05-DEC-1996
29 (viii) ATTORNEY/AGENT INFORMATION:
30 (A) NAME: Perry, Lawrence S.
31 (B) REGISTRATION NUMBER: 31865
32 (C) REFERENCE/DOCKET NUMBER: 766.21
33 (ix) TELECOMMUNICATION INFORMATION:
34 (A) TELEPHONE: (212) 218-2100
35 (B) TELEFAX: (212) 218-2200
36

--> OK

ERRORED SEQUENCES FOLLOW:

545 (2) INFORMATION FOR SEQ ID NO:8:
546 (i) SEQUENCE CHARACTERISTICS:
547 (A) 278 base pairs

↓
LENGTH:

add the MANDATORY leading

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/090,672ADATE: 01/05/2000
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548 (B) TYPE: nucleic acid
549 (C) STRANDEDNESS: double
550 (D) TOPOLOGY: linear
551 (ii) MOLECULE TYPE: cDNA
552 (vi) ORIGINAL SOURCE:
553 (A) ORGANISM: human
554 (G) CELL TYPE: leukocyte
555 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
556 GAAGGAGAAT ATGAAGAGGT TAGAAAAGNT CNGGNTTCTG TTGGTGAAAT GAAGGATGAA 60
557 GGGGAAGAGA CATTAAATTA TCCTGATACT ACCATTGACT TGTCTCACCT TCAACCCCAA 120
558 AGGTCCATCC AGAAATTGGC TTCAAAGAG GAATCTTCTA ATTCTAGTGA CAGTAAATCA 180
559 CAGAGCCGGA GACATTTGTC AGCCAAGGAA AGAAGGGAAA TGAAAAAGAA AAAACTTCCA 240
560 AGTGACTCAG GAGATTTAGA AGCGTTAGAG GGAAAGGA 278
561

1044 (2) INFORMATION FOR SEQ ID NO:36:
1045 (i) SEQUENCE CHARACTERISTICS: *132 listed*
--> 1046 (A) LENGTH: 133 amino acids
--> 1047 (B) ~~SEQUENCE~~ TYPE: amino acid *delete SEQUENCE - just use TYPE*
1048 (D) TOPOLOGY: linear
1049 (ii) MOLECULE TYPE: protein
1050 (vi) ORIGINAL SOURCE:
1051 (A) ORGANISM: human
1052 (G) CELL TYPE: leukocyte
1053 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
1054 Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr
1055 1 5 10 15Pro Thr Ala
1056 Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser *Trinit hard return*
1057 20 25 30 *here*
1058 Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser
1059 35 40 45
1060 Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro
1061 50 55 60
1062 Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys
1063 65 70 75 80
1064 Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu
1065 85 90 95
1066 Ser Leu Glu Pro Ala Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys
1067 100 105 110
1068 Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe
1069 115 120 125
1070 Thr Arg Thr Asp Ile
1071 130
1072

1102 (2) INFORMATION FOR SEQ ID NO:38:
1103 (i) SEQUENCE CHARACTERISTICS:
--> 1104 (A) LENGTH: 128 amino acids
--> 1105 *delete* (B) ~~SEQUENCE~~ TYPE: amino acid
1106 (D) TOPOLOGY: linear
1107 (ii) MOLECULE TYPE: protein
1108 (vi) ORIGINAL SOURCE:
1109 (A) ORGANISM: human

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1110 (G) CELL TYPE: leukocyte
1111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
1112 Met Asp Ala Val Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly
1113 1 5 10 15
1114 Glu Lys Leu Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg
1115 20 25 30
1116 Asp Ser Glu Ser Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His
1117 35 40 45
1118 Gly Tyr Ile Tyr Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp
1119 50 55 60
1120 Ser Ala Glu Thr Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile
1121 65 70 75 80
1122 Lys Asn Leu Ile Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile
1123 85 90 95
1124 Pro Leu Gln Tyr Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln
1125 100 105 110
1126 Gly Thr Thr Gly Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro
1127 115 120 125
1128

1129 (2) INFORMATION FOR SEQ ID NO:39:
--> 1130 (A) ~~(i)~~ LENGTH: 305 base pairs
--> 1131 (B) ~~(A)~~ TYPE: nucleic acid
--> 1132 (C) ~~(B)~~ STRANDEDNESS: double
--> 1133 (D) ~~(C)~~ TOPOLOGY: linear
--> 1134 (E) ~~(D)~~ MOLECULE TYPE: cDNA
1135 (vi) ~~(i)~~ ORIGINAL SOURCE:
1136 (A) ORGANISM: human
1137 (G) CELL TYPE: leukocyte
--> 1138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
--> 1139 TCATGAAGTG AAGCCAAGTG TTTAGACTAG AATGTTATGA GATTAAACCC ACNNNNNNNTT 60
--> 1140 ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGATCTGG ATTTTGTGCA TATGTGGAAT 120
--> 1141 CATAATTTAA ACAAATCAA CTAAGATGAT CCAAGTTCCA CACAACTGCA CTTCAATATT 180
--> 1142 CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCACAAGAT TCTGAGCTGT CGTAAAAAGC 240
--> 1143 CTGGCTCGTG GTTTCTATTT ATAGTG TACA CATGTTGGGT TATAATCACA AACCTGGAAC 300
--> 1144 TCTGT 305
1145

1427 (2) INFORMATION FOR SEQ ID NO:66:
--> 1428 (i) (1) SEQUENCE CHARACTERISTICS:
--> 1429 (A) LENGTH: 22 base pairs
--> 1430 (B) TYPE: nucleic acid
--> 1431 *we* (C) STRANDEDNESS: single
--> 1432 *not* (D) TOPOLOGY: linear
1433 (ii) MOLECULE TYPE: other nucleic acid, synthetic DNA
--> 1434 (1) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1435 GCGTGGAATC AAATGGAGTG GC
1436

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/09/090,672A

DATE: 01/05/2000
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INPUT SET: S34368.raw

Line	Error	Original Text
23	Wrong Classification	(C) CLASSIFICATION: 435
532	Entered (155) and Calc. Seq. Length (278) differ	(A) LENGTH: 155 base pairs
547	Unknown or Misplaced Identifier	(A) 278 base pairs
1046	Entered (133) and Calc. Seq. Length (131) differ	(A) LENGTH: 133 amino acids
1047	Unknown or Misplaced Identifier	(B) SEQUENCE TYPE: amino acid
1104	Entered (128) and Calc. Seq. Length (0) differ	(A) LENGTH: 128 amino acids
1105	Unknown or Misplaced Identifier	(B) SEQUENCE TYPE: amino acid
1130	Unknown or Misplaced Identifier	(i) LENGTH: 305 base pairs
1131	Unknown or Misplaced Identifier	(A) TYPE: nucleic acid
1132	Unknown or Misplaced Identifier	(B) STRANDEDNESS: double
1133	Unknown or Misplaced Identifier	(C) TOPOLOGY: linear
1134	Unknown or Misplaced Identifier	(D) MOLECULE TYPE: cDNA
1138	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1139	Wrong Amino Acid Designator	TCATGAAGTG AAGCCAACTG TTTAGACTAG AATGT
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1140	Wrong Amino Acid Designator	ATTCATAGAC ATAAACCCTC ATTTTAATTA GTGGA
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1141	Wrong Amino Acid Designator	CATAATTTAA ACAAATCAA CTAAGATGAT CCAAG
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1142	Wrong Amino Acid Designator	CAAGTCGGTG TGAAGATGCC TGACTACTGC GTCAC
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1143	Wrong Amino Acid Designator	CTGGCTCGTG GTTTCTATTT ATAGTGTACA CATGTT
1144	Wrong Amino Acid Designator	TCTGT
1419	Entered (24) and Calc. Seq. Length (22) differ	(A) LENGTH: 24 base pairs
1428	Unknown or Misplaced Identifier	(1) SEQUENCE CHARACTERISTICS:
1429	Unknown or Misplaced Identifier	(A) LENGTH: 22 base pairs
1430	Unknown or Misplaced Identifier	(B) TYPE: nucleic acid

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/090,672ADATE: 01/05/2000
TIME: 04:16:27**INPUT SET: S34368.raw**

Line	Error	Original Text
1431	Unknown or Misplaced Identifier	(C) STRANDEDNESS: single
1432	Unknown or Misplaced Identifier	(D) TOPOLOGY: linear
1434	Wrong Or Missing Strandedness Value	(xi)SEQUENCE DESCRIPTION: SEQ ID NO:66:
1434	Wrong or Missing Sequence Topology	(xi)SEQUENCE DESCRIPTION: SEQ ID NO:66: